

SEQUENCE LISTING

<110> Shone, Clifford Charles
Sutton, John Mark

<120> Targeted Agents for Nerve Regeneration

<130> MSQ01-003-US

<140> 10/521,401

<141> 2005-09-12

<150> GB 0216865.6

<151> 2002-07-19

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1

Ile Glu Gly Arg Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile
1 5 10 15

Asp Gln Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu
20 25 30

Ser Lys Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser
35 40 45

Glu Ile Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe
50 55 60

Pro Ser Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn
65 70 75 80

Lys Met Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro
85 90 95

Ala Tyr Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly
100 105 110

Thr Ile Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn
115 120 125

Lys Asp Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val
130 135 140

Ser Gln Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys
 145 150 155 160

Gly Ser Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln
 165 170 175

Leu Glu Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met
 180 185 190

Arg Leu Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met
 195 200 205

Gly Thr Ala Ile Asn Pro Lys
 210 215

<210> 2

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2

Ala Glu Thr Lys Asn Phe Thr Asp Leu Val Glu Ala Thr Lys Trp Gly
 1 5 10 15

Asn Ser Leu Ile Lys Ser Ala Lys Tyr Ser Ser Lys Asp Lys Met Ala
 20 25 30

Ile Tyr Asn Tyr Thr Lys Asn Ser Ser Pro Ile Asn Thr Pro Leu Arg
 35 40 45

Ser Ala Asn Gly Asp Val Asn Lys Leu Ser Glu Asn Ile Gln Glu Gln
 50 55 60

Val Arg Gln Leu Asp Ser Thr Ile Ser Lys Ser Val Thr Pro Asp Ser
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser Ser Ile Thr
 85 90 95

Gly Phe Thr Arg Glu Asp Leu His Met Leu Gln Gln Thr Asn Asn Gly
 100 105 110

Gln Tyr Asn Glu Ala Leu Val Ser Lys Leu Asn Asn Leu Met Asn Ser
 115 120 125

Arg Ile Tyr Arg Glu Asn Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly
 130 135 140

Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Glu Leu Pro Lys
 145 150 155 160

Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Glu Leu Thr Ala Tyr Pro
 165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly
 180 185 190

Ser Val Lys Leu Ser Asp Asn Lys Arg Lys Ile Ile Ile Thr Ala Val
 195 200 205

Val Phe Lys Lys
 210

<210> 3

<211> 636

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 3

Gly Cys Thr Gly Ala Ala Ala Cys Cys Ala Ala Ala Ala Ala Cys Thr
 1 5 10 15

Thr Cys Ala Cys Cys Gly Ala Cys Cys Thr Gly Gly Thr Thr Gly Ala
 20 25 30

Ala Gly Cys Thr Ala Cys Cys Ala Ala Ala Thr Gly Gly Gly Thr
 35 40 45

Ala Ala Cys Thr Cys Thr Cys Thr Gly Ala Thr Cys Ala Ala Ala Thr
 50 55 60

Cys Thr Gly Cys Thr Ala Ala Ala Thr Ala Cys Thr Cys Thr Thr Cys
 65 70 75 80

Thr Ala Ala Ala Gly Ala Cys Ala Ala Ala Ala Thr Gly Gly Cys Thr
 85 90 95

Ala Thr Cys Thr Ala Cys Ala Ala Cys Thr Ala Cys Ala Cys Cys Ala
 100 105 110

Ala Ala Ala Ala Cys Thr Cys Thr Cys Thr Cys Cys Gly Ala Thr
 115 120 125

Cys Ala Ala Cys Ala Cys Cys Cys Gly Cys Thr Gly Cys Gly Thr

130

135

140

Thr Cys Thr Gly Cys Thr Ala Ala Cys Gly Gly Thr Gly Ala Cys Gly
 145 150 155 160

Thr Thr Ala Ala Cys Ala Ala Ala Cys Thr Gly Thr Cys Thr Gly Ala
 165 170 175

Ala Ala Ala Cys Ala Thr Cys Cys Ala Gly Gly Ala Ala Cys Ala Gly
 180 185 190

Gly Thr Thr Cys Gly Thr Cys Ala Gly Cys Thr Gly Gly Ala Cys Thr
 195 200 205

Cys Thr Ala Cys Cys Ala Thr Cys Thr Cys Thr Ala Ala Ala Thr Cys
 210 215 220

Thr Gly Thr Thr Ala Cys Cys Cys Gly Gly Ala Cys Thr Cys Thr
 225 230 235 240

Gly Thr Thr Thr Ala Cys Gly Thr Thr Thr Ala Cys Cys Gly Thr Cys
 245 250 255

Thr Gly Cys Thr Gly Ala Ala Cys Cys Thr Gly Gly Ala Cys Thr Ala
 260 265 270

Cys Cys Thr Gly Thr Cys Thr Thr Cys Thr Ala Thr Cys Ala Cys Cys
 275 280 285

Gly Gly Thr Thr Thr Cys Ala Cys Cys Cys Gly Thr Gly Ala Ala Gly
 290 295 300

Ala Cys Cys Thr Gly Cys Ala Cys Ala Thr Gly Cys Thr Gly Cys Ala
 305 310 315 320

Gly Cys Ala Gly Ala Cys Cys Ala Ala Cys Ala Ala Cys Gly Gly Thr
 325 330 335

Cys Ala Gly Thr Ala Cys Ala Ala Cys Gly Ala Ala Gly Cys Thr Cys
 340 345 350

Thr Gly Gly Thr Thr Cys Thr Ala Ala Ala Cys Thr Gly Ala Ala
 355 360 365

Cys Ala Ala Cys Cys Thr Gly Ala Thr Gly Ala Ala Cys Thr Cys Thr
 370 375 380

Cys Gly Thr Ala Thr Cys Thr Ala Cys Cys Gly Thr Gly Ala Ala Ala

MSQ01-003-US Corrected SEQUENCE LISTING.txt

385	390	395	400
Ala Cys Gly Gly Thr Thr Ala Cys Thr Cys Thr Thr Cys Thr Ala Cys 405 410 415			
Cys Cys Ala Gly Cys Thr Gly Gly Thr Thr Thr Cys Thr Gly Gly Thr 420 425 430			
Gly Cys Thr Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly Gly Thr Cys 435 440 445			
Gly Thr Cys Cys Gly Ala Thr Cys Gly Ala Ala Cys Thr Gly Ala Ala 450 455 460			
Ala Cys Thr Gly Gly Ala Ala Cys Thr Gly Cys Cys Gly Ala Ala Ala 465 470 475 480			
Gly Gly Thr Ala Cys Cys Ala Ala Ala Gly Cys Thr Gly Cys Thr Thr 485 490 495			
Ala Cys Ala Thr Cys Gly Ala Cys Thr Cys Thr Ala Ala Ala Gly Ala 500 505 510			
Ala Cys Thr Gly Ala Cys Cys Gly Cys Thr Thr Ala Cys Cys Cys Cys 515 520 525			
Gly Gly Thr Cys Ala Gly Cys Ala Gly Gly Ala Ala Gly Thr Thr Cys 530 535 540			
Thr Gly Cys Thr Gly Cys Cys Gly Cys Gly Thr Gly Gly Thr Ala Cys 545 550 555 560			
Cys Gly Ala Ala Thr Ala Cys Gly Cys Thr Gly Thr Thr Gly Gly Thr 565 570 575			
Thr Cys Thr Gly Thr Thr Ala Ala Ala Cys Thr Gly Thr Cys Thr Gly 580 585 590			
Ala Cys Ala Ala Cys Ala Ala Ala Cys Gly Thr Ala Ala Ala Ala Thr 595 600 605			
Cys Ala Thr Cys Ala Thr Cys Ala Cys Cys Gly Cys Thr Gly Thr Thr 610 615 620			
Gly Thr Thr Thr Thr Cys Ala Ala Gly Ala Ala Gly 625 630 635			

<210> 4

<211> 212

<212> PRT

<213> Staphylococcus aureus

<400> 4

Ala Asp Val Lys Asn Phe Thr Asp Leu Asp Glu Ala Thr Lys Trp Gly
 1 5 10 15

Asn Lys Leu Ile Lys Gln Ala Lys Tyr Ser Ser Asp Asp Lys Ile Ala
 20 25 30

Leu Tyr Glu Tyr Thr Lys Asp Ser Ser Lys Ile Asn Gly Pro Leu Arg
 35 40 45

Leu Ala Gly Gly Asp Ile Asn Lys Leu Asp Ser Thr Thr Gln Asp Lys
 50 55 60

Val Arg Arg Leu Asp Ser Ser Ile Ser Lys Ser Thr Thr Pro Glu Ser
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Thr Ser Ile Val
 85 90 95

Gly Phe Thr Asn Glu Asp Leu Tyr Lys Leu Gln Gln Thr Asn Asn Gly
 100 105 110

Gln Tyr Asp Glu Asn Leu Val Arg Lys Leu Asn Asn Val Met Asn Ser
 115 120 125

Arg Ile Tyr Arg Glu Asp Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly
 130 135 140

Ala Ala Val Gly Gly Arg Pro Ile Glu Leu Arg Leu Glu Leu Pro Lys
 145 150 155 160

Gly Thr Lys Ala Ala Tyr Leu Asn Ser Lys Asp Leu Thr Ala Tyr Tyr
 165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly
 180 185 190

Ser Val Glu Leu Ser Asn Asp Lys Lys Lys Ile Ile Ile Thr Ala Ile
 195 200 205

Val Phe Lys Lys
 210

<210> 5

<211> 247

<212> PRT

<213> Staphylococcus aureus
<400> 5

Met Lys Arg Lys Leu Phe Phe Lys Ile Ile Phe Val Leu Ser Leu Val
1 5 10 15

Leu Ser Ile His Ser Ile Asn Asp Arg Thr Thr Glu Leu Ser Asn Ile
20 25 30

Ala Leu Ala Asp Asp Val Lys Asn Phe Thr Asp Leu Thr Glu Ala Thr
35 40 45

Asn Trp Gly Asn Lys Leu Ile Lys Gln Ala Asn Tyr Ser Ser Lys Asp
50 55 60

Lys Glu Ala Ile Tyr Asn Tyr Thr Lys Tyr Ser Ser Pro Ile Asn Thr
65 70 75 80

Pro Leu Arg Ser Ser Gln Gly Asp Ile Ser Asn Phe Ser Ala Asp Leu
85 90 95

Gln Glu Lys Ile Leu Arg Leu Asp Arg Leu Ile Ser Lys Ser Ser Thr
100 105 110

Ser Asp Ser Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser
115 120 125

Ser Val Lys Gly Phe Ser Ser Glu Asp Leu Glu Leu Leu Tyr Lys Thr
130 135 140

Glu Asn Gly Lys Tyr Asn Glu Glu Leu Val Lys Lys Leu Asn Asn Ile
145 150 155 160

Met Asn Ser Lys Ile Tyr Thr Glu Tyr Gly Tyr Ser Ser Thr Gln Leu
165 170 175

Val Lys Gly Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Gln
180 185 190

Leu Pro Lys Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Asn Leu Thr
195 200 205

Ala Tyr Pro Gly Gln Gln Glu Ile Leu Leu Pro Arg Gly Thr Asp Tyr
210 215 220

Thr Ile Asn Thr Val Lys Leu Ser Asp Asp His Lys Arg Ile Leu Ile
225 230 235 240

Glu Gly Ile val Phe Lys Lys

245

<210> 6
<211> 211
<212> PRT
<213> Clostridium limosum
<400> 6

Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys
1 5 10 15

Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu
20 25 30

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly
35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu
50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr
65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly
85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys
100 105 110

Thr Ala Phe Glu Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu
115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala
130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala
145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu
165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser
180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile
195 200 205

Asn Pro Lys
210

<210> 7
<211> 160
<212> PRT
<213> Listeria monocytogenes
<400> 7

Asn Lys Ser Leu Lys Phe Thr Ser Leu Glu Glu Ser Glu Lys Trp Gly
1 5 10 15

Ile Asp Gly Phe Ser Val Trp Arg Asn Ser Leu Ser Ser Arg Glu Ile
20 25 30

Gln Ala Ile Arg Asp Tyr Thr Asp Ile Trp His Tyr Gly Asn Met Asn
35 40 45

Gly Tyr Leu Arg Gly Ser Val Glu Lys Leu Ala Pro Asp Asn Ala Glu
50 55 60

Arg Ile Lys Asn Leu Ser Ser Ala Leu Glu Lys Ala Glu Leu Pro Asp
65 70 75 80

Asn Ile Ile Leu Tyr Arg Gly Thr Ser Ser Glu Ile Leu Asp Asn Phe
85 90 95

Leu Asp Leu Lys Asn Leu Asn Tyr Gln Asn Leu Val Gly Lys Thr Ile
100 105 110

Glu Glu Lys Gly Phe Met Ser Thr Thr Ile Ser Asn Gln Thr Phe
115 120 125

Ser Gly Asn Val Thr Met Lys Ile Asn Ala Pro Lys Gly Ser Lys Gly
130 135 140

Ala Tyr Leu Ala His Phe Ser Glu Thr Pro Glu Glu Ala Glu Val Leu
145 150 155 160

<210> 8
<211> 175
<212> PRT
<213> Clostridium acetobutylicum
<400> 8

Thr Asn Met Asp Gln Ala Asn Glu Trp Gly Ser Gln Tyr Tyr Asp Asn
1 5 10 15

Trp Leu Lys Ser Leu Asn Asp Ser Glu Arg Asn Ala Ile Arg Gln Tyr
20 25 30

Thr Gly Asn Asp Tyr Lys Lys Ile Asn Asn Tyr Leu Arg Gly Val Asn
35 40 45

Asp Ser Leu Asp Gly Ile Asp Pro Lys Ile Ile Glu Asp Ile Lys Ser
 50 55 60

Gly Leu Lys Lys Ala Ser Val Pro His Asp Met Lys Val Tyr Arg Gly
 65 70 75 80

Thr Asp Leu Asn Pro Leu Arg Asn Leu Ile Asp Val Gly Lys Asp Gly
 85 90 95

Ser Leu Asp Phe Ser Leu Val Gly Lys Thr Phe Lys Asp Asp Gly Phe
 100 105 110

Met Ser Thr Ala Leu Val Lys Glu Ser Ser Phe Asp Tyr Met Asn Val
 115 120 125

Ser Trp Glu Ile Asn Val Pro Lys Gly Thr Glu Ala Ala Tyr Val Ser
 130 135 140

Lys Ile Ser Tyr Phe Pro Asp Glu Ala Glu Leu Leu Leu Asn His Gly
 145 150 155 160

Gln Glu Met Ile Ile Lys Glu Ala Thr Val Gly Ser Asp Gly Lys
 165 170 175

<210> 9
 <211> 250
 <212> PRT
 <213> Streptococcus pyogenes
 <400> 9

Met Leu Lys Lys Arg Tyr Gln Leu Ala Ile Val Leu Leu Ser Cys
 1 5 10 15

Phe Ser Leu Ile Trp Gln Thr Glu Gly Leu Val Glu Leu Phe Val Cys
 20 25 30

Glu His Tyr Glu Arg Ala Val Cys Glu Gly Thr Pro Ala Tyr Phe Thr
 35 40 45

Phe Ser Asp Gln Lys Gly Ala Glu Thr Leu Ile Lys Lys Arg Trp Gly
 50 55 60

Lys Gly Leu Ile Tyr Pro Arg Ala Glu Gln Glu Ala Met Ala Ala Tyr
 65 70 75 80

Thr Cys Gln Gln Ala Gly Pro Ile Asn Thr Ser Leu Asp Lys Ala Lys
 85 90 95

Gly Glu Leu Ser Gln Leu Thr Pro Glu Leu Arg Asp Gln Val Ala Gln

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100

105

110

Leu Asp Ala Ala Thr His Arg Leu Val Ile Pro Trp Asn Ile Val Val
115 120 125

Tyr Arg Tyr Val Tyr Glu Thr Phe Leu Arg Asp Ile Gly Val Ser His
130 135 140

Ala Asp Leu Thr Ser Tyr Tyr Arg Asn His Gln Phe Asp Pro His Ile
145 150 155 160

Leu Cys Lys Ile Lys Leu Gly Thr Arg Tyr Thr Lys His Ser Phe Met
165 170 175

Ser Thr Thr Ala Leu Lys Asn Gly Ala Met Thr His Arg Pro Val Glu
180 185 190

Val Arg Ile Cys Val Lys Lys Gly Ala Lys Ala Ala Phe Val Glu Pro
195 200 205

Tyr Ser Ala Val Pro Ser Glu Val Glu Leu Leu Phe Pro Arg Gly Cys
210 215 220

Gln Leu Glu Val Val Gly Ala Tyr Val Ser Gln Asp Gln Lys Lys Leu
225 230 235 240

His Ile Glu Ala Tyr Phe Lys Gly Ser Leu
245 250

<210> 10

<211> 250

<212> PRT

<213> Streptococcus pyogenes

<400> 10

Met Leu Lys Lys Arg Tyr Gln Leu Ala Ile Val Leu Leu Ser Cys
1 5 10 15

Phe Ser Leu Ile Trp Gln Thr Glu Gly Leu Val Glu Leu Phe Val Cys
20 25 30

Glu His Tyr Glu Arg Ala Val Cys Glu Gly Thr Pro Ala Tyr Phe Thr
35 40 45

Phe Ser Asp Gln Lys Gly Ala Glu Thr Leu Ile Lys Lys Arg Trp Gly
50 55 60

Lys Gly Leu Ile Tyr Pro Arg Ala Glu Gln Glu Ala Met Ala Ala Tyr
65 70 75 80

Thr Cys Gln Gln Ala Gly Pro Ile Asn Thr Ser Leu Asp Lys Ala Lys
 85 90 95

Gly Glu Leu Ser Gln Leu Thr Pro Glu Leu Arg Asp Gln Val Ala Gln
 100 105 110

Leu Asp Ala Ala Thr His Arg Leu Val Ile Pro Trp Asn Ile Val Val
 115 120 125

Tyr Arg Tyr Val Tyr Glu Thr Phe Leu Arg Asp Ile Gly Val Ser His
 130 135 140

Ala Asp Leu Thr Ser Tyr Tyr Arg Asn His Gln Phe Asp Pro His Ile
 145 150 155 160

Leu Cys Lys Ile Lys Leu Gly Thr Arg Tyr Thr Lys His Ser Phe Met
 165 170 175

Ser Thr Thr Ala Leu Lys Asn Gly Ala Met Thr His Arg Pro Val Glu
 180 185 190

Val Arg Ile Cys Val Lys Lys Gly Ala Lys Ala Ala Phe Val Glu Pro
 195 200 205

Tyr Ser Ala Val Pro Ser Glu Val Glu Leu Leu Phe Pro Arg Gly Cys
 210 215 220

Gln Leu Glu Val Val Gly Ala Tyr Val Ser Gln Asp Gln Lys Lys Leu
 225 230 235 240

His Ile Glu Ala Tyr Phe Lys Gly Ser Leu
 245 250

<210> 11
 <211> 855
 <212> PRT
 <213> Clostridium botulinum
 <400> 11

Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp
 1 5 10 15

Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro Phe Ile Gly Asp
 20 25 30

Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys Asp Ile Asn Glu
 35 40 45

Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser Val Asp Gln Val

MSQ01-003-US Corrected SEQUENCE LISTING.txt

50

55

60

Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu Asp Leu Leu Tyr
 65 70 75 80

Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly Glu Asn Gln Val
 85 90 95

Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu Asn Ser Tyr Tyr
 100 105 110

Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu Asp Phe Thr Phe
 115 120 125

Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala Lys Val Tyr Thr
 130 135 140

Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly Val Gln Gly Gly
 145 150 155 160

Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp Phe Thr Thr Asn
 165 170 175

Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp Val Ser Ala Ile
 180 185 190

Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn Ser Val Arg Arg
 195 200 205

Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val Thr Ile Leu Leu
 210 215 220

Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Ala Phe Val Ile
 225 230 235 240

Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys Thr Ile Asp Asn
 245 250 255

Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser Tyr Glu Trp Met
 260 265 270

Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe Asn Asn Ile Ser
 275 280 285

Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly Ala Ile Lys Ala
 290 295 300

Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp Lys Glu Asn

MSQ01-003-US Corrected SEQUENCE LISTING.txt

305

310

315

320

Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile
 325 330 335

Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val
 340 345 350

Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp Glu Leu Asn
 355 360 365

Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn Leu Ile Asp Ser
 370 375 380

His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu Lys Ala Lys Val
 385 390 395 400

Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr
 405 410 415

Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile
 420 425 430

Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val
 435 440 445

Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln
 450 455 460

Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu
 465 470 475 480

Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn
 485 490 495

Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys
 500 505 510

Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn
 515 520 525

Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr
 530 535 540

Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp
 545 550 555 560

Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val

MSQ01-003-US Corrected SEQUENCE LISTING.txt

565

570

575

Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu
 580 585 590

Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys
 595 600 605

Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr
 610 615 620

Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe
 625 630 635 640

Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu
 645 650 655

Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr
 660 665 670

Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met
 675 680 685

Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn
 690 695 700

Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn
 705 710 715 720

Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met
 725 730 735

Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met
 740 745 750

Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg
 755 760 765

Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro
 770 775 780

Met Asn Asn Thr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe
 785 790 795 800

Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe
 805 810 815

Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val

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820

825

830

Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp
835 840 845

Gly Phe Val Pro Val Ser Glu
850 855

<210> 12
<211> 454
<212> PRT
<213> Clostridium botulinum
<400> 12

Gly Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn
1 5 10 15

Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn
20 25 30

Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp
35 40 45

Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu
50 55 60

Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp
65 70 75 80

Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser
85 90 95

Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp
100 105 110

Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn
115 120 125

Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu
130 135 140

Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile
145 150 155 160

Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr
165 170 175

Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile
180 185 190

Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr
 195 200 205

Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser
 210 215 220

Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala
 225 230 235 240

Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln
 245 250 255

Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn
 260 265 270

Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr
 275 280 285

Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp
 290 295 300

Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr
 305 310 315 320

Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr
 325 330 335

Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr
 340 345 350

Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu
 355 360 365

Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met
 370 375 380

Asn Asn Thr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn
 385 390 395 400

Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg
 405 410 415

Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys
 420 425 430

Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly
 435 440 445

Phe Val Pro Val Ser Glu
450

<210> 13
<211> 1066

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 13

Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys
1 5 10 15

Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu
20 25 30

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly
35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu
50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr
65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly
85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys
100 105 110

Thr Ala Phe Glu Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu
115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala
130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala
145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu
165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser
180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile
195 200 205

Asn Pro Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys
 210 215 220

Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro Phe
 225 230 235 240

Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys Asp
 245 250 255

Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser Val
 260 265 270

Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu Asp
 275 280 285

Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly Glu
 290 295 300

Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu Asn
 305 310 315 320

Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu Asp
 325 330 335

Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala Lys
 340 345 350

Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly Val
 355 360 365

Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp Phe
 370 375 380

Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp Val
 385 390 395 400

Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn Ser
 405 410 415

Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val Thr
 420 425 430

Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Ala
 435 440 445

Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys Thr
 450 455 460

Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser Tyr
465 470 475 480

Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe Asn
485 490 495

Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly Ala
500 505 510

Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp
515 520 525

Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp
530 535 540

Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu
545 550 555 560

Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp
565 570 575

Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn Leu
580 585 590

Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu Lys
595 600 605

Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe
610 615 620

Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe
625 630 635 640

Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn
645 650 655

Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly
660 665 670

Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser
675 680 685

Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile
690 695 700

Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg
705 710 715 720

Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser
725 730 735

Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu
740 745 750

Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe
755 760 765

Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe
770 775 780

Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn
785 790 795 800

Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn
805 810 815

Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly
820 825 830

Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe
835 840 845

Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe
850 855 860

Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp
865 870 875 880

Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn
885 890 895

Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg
900 905 910

Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile
915 920 925

Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Asp Ile Leu Tyr
930 935 940

Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn
945 950 955 960

Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile
965 970 975

Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln
 980 985 990

Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys
 995 1000 1005

Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly
 1010 1015 1020

Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr
 1025 1030 1035

Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu
 1040 1045 1050

Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu
 1055 1060 1065

<210> 14

<211> 1067

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 14

Ala Glu Thr Lys Asn Phe Thr Asp Leu Val Glu Ala Thr Lys Trp Gly
 1 5 10 15

Asn Ser Leu Ile Lys Ser Ala Lys Tyr Ser Ser Lys Asp Lys Met Ala
 20 25 30

Ile Tyr Asn Tyr Thr Lys Asn Ser Ser Pro Ile Asn Thr Pro Leu Arg
 35 40 45

Ser Ala Asn Gly Asp Val Asn Lys Leu Ser Glu Asn Ile Gln Glu Gln
 50 55 60

Val Arg Gln Leu Asp Ser Thr Ile Ser Lys Ser Val Thr Pro Asp Ser
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser Ser Ile Thr
 85 90 95

Gly Phe Thr Arg Glu Asp Leu His Met Leu Gln Gln Thr Asn Asn Gly
 100 105 110

Gln Tyr Asn Glu Ala Leu Val Ser Lys Leu Asn Asn Leu Met Asn Ser

MSQ01-003-US Corrected SEQUENCE LISTING.txt

115

120

125

Arg Ile Tyr Arg Glu Asn Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly
 130 135 140

Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Glu Leu Pro Lys
 145 150 155 160

Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Glu Leu Thr Ala Tyr Pro
 165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly
 180 185 190

Ser Val Lys Leu Ser Asp Asn Lys Arg Lys Ile Ile Ile Thr Ala Val
 195 200 205

Val Phe Lys Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn
 210 215 220

Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro
 225 230 235 240

Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys
 245 250 255

Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser
 260 265 270

Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu
 275 280 285

Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly
 290 295 300

Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu
 305 310 315 320

Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu
 325 330 335

Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala
 340 345 350

Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly
 355 360 365

Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp

MSQ01-003-US Corrected SEQUENCE LISTING.txt

370

375

380

Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp
 385 390 395 400

Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn
 405 410 415

Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val
 420 425 430

Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly
 435 440 445

Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys
 450 455 460

Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser
 465 470 475 480

Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe
 485 490 495

Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly
 500 505 510

Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser
 515 520 525

Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu
 530 535 540

Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg
 545 550 555 560

Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile
 565 570 575

Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn
 580 585 590

Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu
 595 600 605

Lys Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile
 610 615 620

Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr

MSQ01-003-US Corrected SEQUENCE LISTING.txt

625

630

635

640

Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys
645 650 655

Asn Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu
660 665 670

Gly Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly
675 680 685

Ser Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn
690 695 700

Ile Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile
705 710 715 720

Arg Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp
725 730 735

Ser Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe
740 745 750

Leu Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn
755 760 765

Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe
770 775 780

Phe Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile
785 790 795 800

Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile
805 810 815

Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr
820 825 830

Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp
835 840 845

Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu
850 855 860

Phe Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn
865 870 875 880

Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu

885

890

895

Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg
 900 905 910

Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg
 915 920 925

Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu
 930 935 940

Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys
 945 950 955 960

Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala
 965 970 975

Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe
 980 985 990

Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe
 995 1000 1005

Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile
 1010 1015 1020

Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn
 1025 1030 1035

Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu
 1040 1045 1050

Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu
 1055 1060 1065

<210> 15

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 15

Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys
 1 5 10 15

Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu
 20 25 30

MSQ01-003-US Corrected SEQUENCE LISTING.txt

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly
35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu
50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr
65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly
85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys
100 105 110

Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu
115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala
130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala
145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu
165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser
180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile
195 200 205

Asn Pro Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys
210 215 220

Thr Leu Asp Cys Gly Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe
225 230 235 240

Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe
245 250 255

Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn
260 265 270

Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly
275 280 285

MSQ01-003-US Corrected SEQUENCE LISTING.txt

Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser
290 295 300

Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile
305 310 315 320

Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg
325 330 335

Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser
340 345 350

Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu
355 360 365

Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe
370 375 380

Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe
385 390 395 400

Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn
405 410 415

Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn
420 425 430

Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly
435 440 445

Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe
450 455 460

Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe
465 470 475 480

Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp
485 490 495

Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn
500 505 510

Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg
515 520 525

Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile
530 535 540

MSQ01-003-US Corrected SEQUENCE LISTING.txt

Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr
545 550 555 560

Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn
565 570 575

Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile
580 585 590

Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln
595 600 605

Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys
610 615 620

Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr
625 630 635 640

Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val
645 650 655

Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser
660 665 670

Thr His Trp Gly Phe Val Pro Val Ser Glu
675 680

<210> 16

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 16

Cys Ser Ala Ile Glu Gly Arg Ala Pro Gly Ile Cys
1 5 10

<210> 17

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17

Cys Gly Ile Glu Gly Arg Ala Pro Gly Pro Gly Ser Ser Val Gly Ser
1 5 10 15

Ser Leu Ser Cys
20

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 18

Cys Gly Leu Val Pro Arg Gly Ser Gly Pro Cys
1 5 10

<210> 19
<211> 20
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 19

Cys Gly Leu Val Pro Arg Gly Ser Gly Pro Gly Ser Ser Val Gly Ser
1 5 10 15

Ser Leu Ser Cys
20

<210> 20
<211> 13
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 20

Cys Lys Ser Asp Asp Asp Asp Lys Ala Pro Gly Ile Cys
1 5 10

<210> 21
<211> 22
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 21

Cys Lys Ser Glu Glu Lys Leu Tyr Asp Asp Asp Asp Lys Asp Arg Trp
1 5 10 15

Gly Ser Ser Arg Ile Cys
20

<210> 22
<211> 17

MSQ01-003-US Corrected SEQUENCE LISTING.txt

<212> PRT
<213> Clostridium Botulinum
<400> 22

Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp
1 5 10 15

Cys

<210> 23
<211> 10
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 23

Cys Gly Leu Val Pro Ala Gly Ser Gly Pro
1 5 10

<210> 24
<211> 17
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 24

Cys Gly Leu Val Pro Ala Gly Ser Gly Pro Ser Ala Gly Ser Ser Ala
1 5 10 15

Cys

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 25

Gly Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 26

MSQ01-003-US Corrected SEQUENCE LISTING.txt

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 27

Pro Pro Pro Ile Glu Gly Arg
1 5

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)
Clifford Charles Shone et al.)
International Application No. PCT/GB03/03082) Examiner: Brian J. Gangle
Application No.: 10/521,401) Group Art Unit: 1645
International Filing Date: July 15, 2003) Confirmation No.: 2849

For **TARGETED AGENTS FOR NERVE
REGENERATION**

STATEMENT ACCORDING TO 37 C.F.R. § 1.821(f)

M.S. – SEQUENCE LISTING
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

Submitted herewith is a sequence listing as part of the above-captioned patent application. Applicants' representative states that the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are identical.

Applicants' representative hereby verifies that the information on the accompanying computer readable copy is identical to the paper copy of the sequence listing. The enclosed sequence listing does not include any new matter that goes beyond the disclosure in the above-captioned application as filed.

Respectfully submitted,


Daniel W. Celander, Ph.D.
Registration No. 52,710

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